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Poster Abstracts

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INRA Early Career Award Winner

Impact on plant microbiota and plant health of a recent shift in rice genetic diversity in a sustainable and century-old Chinese rice agrosystem

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Plant microbial communities may moderate the plant responses to different abiotic or biotic stresses like pathogens. On the other hand, plant genotypes may influence the composition and structure of the plant microbiota. In the Chinese Yuanyang terraces (YYT), a sustainable rice disease control has been achieved for centuries using mixtures of traditional genetically diverse rice varieties harboring a wide panel of resistance genes. However, this centuries-old agrosystem is currently challenged by the introduction of several “modern” rice varieties. The potential simplification of the rice varietal landscape is likely to drive a modification of the rice microbiota, which may have an impact on the plant-pathogen dynamics, and further on the frequency, extent and impact of disease emergence events. We here investigated the microbial communities (bacteria, fungi and viruses) associated with roots and aerial organs from eleven and eight YYT fields cultivated with traditional and “modern” rice varieties, respectively. Besides using a genotyping-by-sequencing approach (GBS) to decipher the rice genetic diversity, microbial communities were characterized by metagenomics approaches. The GBS approach confirms a shift of the rice genetic diversity and split the varieties into three lineages (traditional varieties, “modern” introduced varieties and one Japonica traditional variety). Metagenomics approaches show that microbial communities from aerial organs are lineage-dependent and that microbial communities from the roots are more homogeneous and not different among rice lineages. Interestingly, our study reveals a high prevalence (15%) of Southern rice black-streaked dwarf virus in Yuanyang terraces, and that this virus is significantly more prevalent in traditional local varieties.

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Transcriptome profiling of the endophyte Methylobacterium mesophilicum during Citrus sinensis roots interaction

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Methylobacterium genus has been found in association with a range of plant species. In this work we focused on evaluating the initial step of M. mesophilicum colonization in Citrus sinensis roots, since in previous work we verified that this association improves Citrus development. Here using CG-MS we demonstrated that metabolic compounds from citrus root exudates are modified in presence of M. mesophilicum. Using global gene expression analysis, we identify key genes from M. mesophilicum regulated during two different steps of the colonization: i. Plant recognition and ii. Plant colonization. The present study shows that genes related to energy production, stress and amino acid transport were down regulated in both step evaluated, and genes related to peptidoglycan biosynthesis, plant interaction and thioreodoxin and specially sugar transporter were up regulated. The up regulation of sugar transporter together with the presence of sugar compounds (fructose, arabinose and maltose) produced by the host plant exclusively in the presence of the bacteria, strongly indicates that these sugars are key compounds in first steps of M. mesophilicum SR1.6/6 – citrus interaction. These results contribute to understand the first step of citrus-M. mesophilicum interaction.